

Best Local Similarity: 85.19% Mismatches: 0
Query Match: 81.68% Indels: 20
DB: 9 Gaps: 1

US-10-005-907-2 (1-135) x AK126682 (1-4032)

QY 1 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys 20
DB 377 ATGGGAATTAATCTCTGGGAAACTC----- 403

QY 21 LysGlyAsnProLysGluArgLysArgGlnGluMetThrThrPheGluArgLysLeu 40
DB 404 -----AGGAGGAATGACTACTTTGAGAAACTT 436

QY 41 GlnPheArgLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGlu 60
DB 437 CAGCAAGATAGAAAGCCGAGAGTTTCTCATCTTCTATACGGAACGAGAAAT 496

QY 61 GlySerLysSerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer 80
DB 497 GGCAGTCTCTCAGGAAGTGTCTACACTGTCTATTATCATCTCCCTCATCAGATCC 556

QY 81 SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
DB 557 TCCCTGAGTCATGATGATGCTATGAGACATGCTCTCCCTCAGGAAAGTGAGA 616

QY 101 GlnPheArgLysSerGlnGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro 120
DB 617 CAGTTAGGAAGTGTAGAGACAGATATGCCCTTCTTAGGACTTCTGTAGTAGGCTT 676

QY 121 CysSerCysThrHisGlnHisAspTyrGluValValPheProHis 135
DB 677 TGTCTCTGACCCATGAGCATGATTATGAGTGTGTGTTTCCAC 721

RESULT 6
AK124520 4136 bp mRNA linear PRI 09-SEP-2003
LOCUS Homo sapiens cDNA FLJ4529 f1a, clone BRACE3002390.
DEFINITION AK124520
ACCESSION AK124520
VERSION AK124520.1 GI:34530324
KEYWORDS oligo capping f1a (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS
Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuma, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yanashita, H., Matsumoto, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kawahori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagata, K., Masuno, Y., Nagai, K. and Inogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 4136)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI); (supported by Japan
Key Technology Center etc.); 5' & 3' end one pass sequencing: RAB
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers
1. 4136
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRACE3002390"
/tissue_type="cerebellum"
/clone_lib="BRACE3"
/notes="cloning vector: pWE18SFL3"
136.537
/notes="unnamed protein product"
/codon_start=1
/protein_id="BAC85873.1"
/db_xref="GI:34530325"
/translation="MVMLEDNSSTGGGARNVCELVFLVLCQGRKQKQMTQOAG
PMLRGRBRASSSTNPGTLILDFOSEPPLAARGQHEPVRNCVLPHPAFSSKCPGQ
YFFPKSETQELNRVTVKRWELIISSENSGRK"

CDS

Alignment Scores:
Pred. No.: 436-51 Length: 4136
Score: 581.00 Matches: 114
Conservative: 1
Percent Similarity: 85.19% Mismatches: 0
Best Local Similarity: 84.44% Indels: 20
Query Match: 81.26% Gaps: 1
DB: 9

US-10-005-907-2 (1-135) x AK124520 (1-4136)

QY 1 MetGlyAsnTyrLeuLeuArgLysLeuSerCysLeuGlyGluAsnGlnLysLysProLys 20
DB 498 ATGGGAATTAATCTCTGGGAAACTC----- 524

QY 21 LysGlyAsnProLysGluArgLysArgGlnGluMetThrThrPheGluArgLysLeu 40
DB 525 -----AGGAGGAATGACTACTTTGAGAAACTT 557

QY 41 GlnPheArgLysLysSerGlnGluValSerSerThrSerAsnGlnGluAsnGlu 60
DB 558 CAGCAAGATAGAAAGCCGAGAGTTTCTCATCTTCTATACGGAACGAGAAAT 617

QY 61 GlySerLysSerGluGluValCysTyrThrValIleAsnHisIleProHisGlnArgSer 80
DB 618 GGCAGTCTCTCAGGAAGTGTCTACACTGTCTATTATCATCTCCCTCATCAGAAATCC 677

QY 81 SerLeuSerSerAsnAspAspGlyTyrGluAsnIleAspSerLeuThrArgLysValArg 100
DB 678 TCCCTGAGTCATGATGATGCTATGAGACATGCTCTCCCTCAGGAAAGTGAGA 737

QY 101 GlnPheArgLysSerGluThrGluTyrAlaLeuLeuArgThrSerValSerArgPro 120
DB 738 CAGTTAGGAAGTGTAGAGACAGATATGCCCTTCTTAGGACTTCTGTAGTAGGCTT 797

QY 121 CysSerCysThrHisGlnHisAspTyrGluValValPheProHis 135
DB 798 TGTCTCTGACCCATGAGCATGATTATGAGTGTGTGTTTCCAC 842

RESULT 7
AC074365/c AC074365 141268 bp DNA linear HTG 23-SEP-2000
LOCUS Homo sapiens chromosome 1 clone RP11-11524, WORKING DRAFT SEQUENCE,
DEFINITION 10 unordered pieces.
ACCESSION AC074365
VERSION AC074365.5 GI:10280935
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 141268)
Waterston, R.H.
AUTHORS The sequence of Homo sapiens clone
TITLE Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 141268)
Waterston, R.H.

TITLE Direct Submission
JOURNAL Submitted (29-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT On Sep 23, 2000 this sequence version replaced gi:9838075.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 ----- Project Information -----
 Center Project name: H.NH0115C04
 ----- Summary Statistics -----

Sequencing vector: M13, 100%
 Sequencing vector: Plasmid, 0%
 Chemistry: Dye-terminator Big Dye, 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 136274 bases at least Q40
 Consensus quality: 138356 bases at least Q30
 Consensus quality: 139182 bases at least Q20
 Insert size: 142000; agarose-fp
 Insert size: 1420368; sum-of-contigs
 Quality coverage: 4.64 in Q20 bases; agarose-fp
 Quality coverage: 4.81 in Q20 bases; sum-of-contigs

 NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 31377: contig of 31377 bp in length
 * 31378 31477: gap of unknown length
 * 31478 63011: contig of 31534 bp in length
 * 63012 63111: gap of unknown length
 * 63112 64845: contig of 1734 bp in length
 * 64846 64945: gap of unknown length
 * 64946 67606: contig of 2661 bp in length
 * 67607 67706: gap of unknown length
 * 67707 77674: contig of 9968 bp in length
 * 77675 77774: gap of unknown length
 * 77775 89256: contig of 11482 bp in length
 * 89257 89357: gap of unknown length
 * 89357 100400: contig of 11044 bp in length
 * 100401 100500: gap of unknown length
 * 100501 11915: contig of 11415 bp in length
 * 11916 112015: gap of unknown length
 * 112016 125713: contig of 13698 bp in length
 * 125714 125814: gap of unknown length
 * 125814 141268: contig of 15455 bp in length.

FEATURES

source
 1..141268
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP11-115C4"

misc_feature
 1..31377
 /note="assembly_name:Contig10"
 31478..63011
 /note="assembly_name:Contig11"
 63112..64845
 /note="assembly_name:Contig2"
 64946..67606
 /note="assembly_name:Contig3"
 67707..77674
 /note="assembly_name:Contig4"
 77775..89256
 /note="assembly_name:Contig5"
 89357..100400

misc_feature
 100501..111915
 /note="assembly_name:Contig6"
 misc_feature
 112016..125713
 /note="assembly_name:Contig7"
 misc_feature
 125814..141268
 /note="assembly_name:Contig8"
 misc_feature
 125814..141268
 /note="assembly_name:Contig9"
 clone_end:SP6
 vector_side:left

ORIGIN

Alignment Scores:
 Pred. No.: 1.59e-33 Length: 141268
 Score: 430.00 Matches: 80
 Percent Similarity: 100.00% Conservatively: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 60.14% Indels: 0
 DB: 2 Gaps: 0

US-10-005-907-2 (1-136) x AC074365 (1-141268)

QY 56 GlnGluAndGluAsnGlySerGlySerGluGluValGlyThrValIleLeuHisIle 75
 DB 5700 CAGGAAACGAGATGGCAGTGGTCTCGAAGATGGTCTGCTATATCATC 5641
 QY 76 ProHisGlnArgSerSerLeuSerSerSerSerSerSerSerSerSerSerSer 95
 DB 5640 CCCATCAGATGCTCCCTGAGCTCCATGATGATGATGATGATGATGATGATG 5581
 QY 96 ThrArgLysValArgGlnPheArgGluArgSerGluThrGluThrAlaLeuLeuArgThr 115
 DB 5580 ACAAGGAAGTGGACAGATTTAGAGAAAGGTGACAGACAGATATGCCCTTCTTAG 5521
 QY 116 SerValSerArgProCysSerCysThrHisGluHisAspTyrGluValValPheProHis 135
 DB 5520 TCTGTATTAGGCTTTCTCTGACCCATGATGATGATGATGATGATGATGATG 5461

RESULT 8

AL606804
 LOCUS Human DNA sequence from clone RP11-978115 on chromosome 1, complete
 DEFINITION sequence.

ACCESSION AL606804
 VERSION AL606804.11 GI:24366459
 KEYWORDS HTG
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases) to 185467
 Almeida J.
 Direct Submission

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Submitted (16-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Oct 24, 2002 this sequence version replaced gi:18121511.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone, and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

FEATURES
source

Location/Qualifiers
1. 527
/organism="Homo sapiens"
/db_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4109064"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 55"
/notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcccttcggcc); Site 2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCACATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 100.0%; Score 405; DB 10; Length 527;
Best Local Similarity 100.0%; Pred. No. 6.1e-86;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAATATCTCTCGAAACTCAGTTGCTGGGAGAGATCAAAAGAGCCCAAG 60
DB 45 ATGGGAATATCTCTCGAAACTCAGTTGCTGGGAGAGATCAAAAGAGCCCAAG 104
QY 61 AAGGAACCCGATGAG 120
DB 105 AAGGAACCCGATGAG 164
QY 121 CAAGATCAAGATAG 180
DB 165 CAAGATCAAGATAG 224
QY 181 GGCAGTGGTTCGAG 240
DB 225 GGCAGTGGTTCGAG 284
QY 241 TCCTGAGCTCAAGATGAG 300
DB 285 TCCTGAGCTCAAGATGAG 344
QY 301 CAGTTTAG 360
DB 345 CAGTTTAG 404
QY 361 TGTTCTGACCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 405
DB 405 TGTTCTGACCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 449

RESULT 2

LOCUS AM480906 298 bp mRNA linear EST 09-JUL-2000
DEFINITION 3316 MARC 2P1G Sus scrofa CDNA 5', mRNA sequence.
ACCESSION AM480906
VERSION AM480906.1 GI:7050949
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Pahrenkrug, S.C., Smith, T.P.L., Preking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keese, J.W.
TITLE Porcine gene discovery by normalized cDNA-library sequencing and ZST cluster assembly

JOURNAL
MEDLINE
PUBMED
COMMENT

Mamm. Genome 13 (6), 475-478 (2002)
22213789
12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 19 row: F column: 21
Seq primer: ATTAGGTGACACTATAG.

FEATURES
source

Location/Qualifiers
1. 288
/organism="Sus scrofa"
/db_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2P1G"
/note="Vector: PCMV SPORTS; Site 1: NotI; Site 2: SalI; library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Query Match 16.0%; Score 64.8; DB 10; Length 288;
Best Local Similarity 75.8%; Pred. No. 4e-05;
Matches 94; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 285 CACAGGAAAGTGAGACAGTTTATGAGAAAGTTCAGAGACAGATATGCCCTTCTTAGGAC 344
DB 2 CACAGAGAGTGAGACCATTAAGCGAGGATCAGAACAGATATGCCCTTCTTAGGAC 61
QY 345 TTCCTGTAGT---AGGCTTGTTCACCCAGATGATGATGATGATGATGATGATGATG 401
DB 62 GACTTACATCCCAAGTTTCTCTCTATACCCCTGAGATGATGATGATGATGATGATG 121
QY 402 ACAC 405
DB 122 TCAC 125

RESULT 3

LOCUS BF797507 1045 bp mRNA linear EST 12-JAN-2001
DEFINITION 60225174F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4340323 5', mRNA sequence.
ACCESSION BF797507
VERSION BF797507.1 GI:12102561
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1045)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: c9pbbs@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM9852 row: d column: 20

/gene="GAP-1"
 /note="Homology region A with Elk-1 protein (Ets domain)
 is bp 130-147, amino acids 1-89; Homology region B with
 Elk-1 protein, required for cooperative ternary complex
 formation with SRF is bp 565-617, amino acids 136-157.
 Sequence diverges from SRF-18 at bp 1223, amino acid 160;
 Homology region C with Elk-1 protein, core of regulated
 transcription activation domain, is bp 1203-1355; amino
 acids 352-402; (S/T/P motifs conserved between SRF-1A and
 Elk-1 are located at amino acids 7354, 7361, 7366, 5381,
 8387, 7420, 8425, corresponding to bp 1209-1214, bp
 1230-1235, bp 1245-1250, bp 1290-1295, bp 1308-1313, bp
 1407-1412, bp-1432-1427"
 /codon_start=1
 /product="GAP-1A protein"
 /protein_id="AA043631.1"

FEATURES

Source

Location/Qualifiers

1. 527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4109064"
/tissue_type="from acute myelogenous leukemia"
/lab_host="PH108 (T1 phage-resistant)"
/clone_lib="NTH MGC 55"
/notes="Organ: Bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccatcgcc); Site 2: SfiI (ggccatcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 100.0%; Score 405; DB 10; Length 527;
Best Local Similarity 100.0%; Fred. No. 6.1e-86;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGAATATCTCTCGGAAAACCTGCTTCCTGGGAGAGATCAAAAGAGCCCAAG 50
DB 45 ATGGGAATATCTCTCGGAAAACCTGCTTCCTGGGAGAGATCAAAAGAGCCCAAG 104
QY 61 AAAGCAACCCAGATGAGGAAAGAAACCGCAGGAATGACTACATTTGAAAGAAACTT 120
DB 105 AAAGCAACCCAGATGAGGAAAGAAACCGCAGGAATGACTACATTTGAAAGAAACTT 164
QY 121 CAAGATCAAGATAGAAAGCCAGGAAGTTTCATCCACTTCTAATCAGGAAACGAGAT 180
DB 165 CAAGATCAAGATAGAAAGCCAGGAAGTTTCATCCACTTCTAATCAGGAAACGAGAT 224
QY 181 GCGATGTTCTGAGAGTGTGTACATGTCATTATATCAATCCCATCAGAGATCC 240
DB 225 GCGATGTTCTGAGAGTGTGTGTACATGTCATTATATCAATCCCATCAGAGATCC 284
QY 241 TCCTGAGCTCCGATGATGCTGATGAGAACTTGTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 285 TCCTGAGCTCCGATGATGCTGATGAGAACTTGTCTCTCTCTCTCTCTCTCTCTCTCT 344
QY 301 CAGTTTAGAAGAGCTCAGACAGAGATATGCCCTTCTTAGGACTTCTTTAGTAGCCT 360
DB 345 CAGTTTAGAAGAGCTCAGACAGAGATATGCCCTTCTTAGGACTTCTTTAGTAGCCT 404
QY 361 TGTCTCTGACCCATGAGCATGATTATGAGTTGTGTTTCCAC 405
DB 405 TGTCTCTGACCCATGAGCATGATTATGAGTTGTGTTTCCAC 449

RESULT 2

AW480906 288 bp mRNA linear Ref 09-JUL-2000
LOCUS 33516 MARC 2P-G Sus scrofa cDNA 5', mRNA sequence
DEFINITION
ACCESSION AW480906
VERSION AW480906.1 GI:7050949
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Fahrbrugg S.C., Smith T.P.L., Fekking B.A., Cho J., White J.,
Vallet J., Wisniewski R., Rohrer G.A., Pertea G., Sultana R.,
Quackenbush J. and Keefe J.W.
TITLE Porcine gene discovery by normalized cDNA-library sequencing and
Ref cluster assembly